





















FIGURE 10

FIGURE 10A

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
At1g08660/F22O13.14	<i>Arabidopsis thaliana</i>	n.d.	AC003981 AAF99778.1 AY064135 AAL36042.1 AY124807 AAM70516.1 NC_003070 NP_172342.1 NM_180609 NP_850940.1	Q8VZJ0 Q9FRR9	
$\alpha$ -2,3-sialyltransferase (ST3Gal-IV)	<i>Bos taurus</i>	n.d.	AJ584673 CAE48298.1		
$\alpha$ -2,6-sialyltransferase (Siat7b)	<i>Bos taurus</i>	n.d.	AJ620651 CAF05850.1		
$\alpha$ -2,8-sialyltransferase (Siat8D)	<i>Bos taurus</i>	n.d.	AJ699421 CAG27883.1		
CMP $\alpha$ -2,6-sialyltransferase (ST6Gal I)	<i>Bos taurus</i>	2.4.99.1	Y15111 CAA75385.1 NM_177517 NP_803483.1	O18974	
sialyltransferase ST3Gal-II (Siat4B)	<i>Bos taurus</i>	n.d.	AJ748841 CAG44450.1		
sialyltransferase ST3Gal-VI (Siat10)	<i>Bos taurus</i>	n.d.	AJ748843 CAG44452.1		
ST6GalNAc-VI	<i>Bos taurus</i>	n.d.	AJ620949 CAF06586.1		
polysialyltransferase (PST) (fragment) ST8Sia IV	<i>Cercopithecus aethiops</i>	2.4.99.-	AF210729 AAF17105.1	Q9TT09	
$\alpha$ -2,3-sialyltransferase ST3Gal I (Siat4)	<i>Clona intestinalis</i>	n.d.	AJ626815 CAF25173.1		
$\alpha$ -2,8-polysialyltransferase ST8Sia IV	<i>Cricetulus griseus</i>	2.4.99.-	-AAE28634 Z46801 CAA86822.1	Q64690	
Gal $\beta$ -1,3/4-GlcNAc $\alpha$ -2,3-sialyltransferase ST3Gal II (fragment)	<i>Cricetulus griseus</i>	n.d.	AY266676 AAP22943.1	Q80WK9	
$\alpha$ -2,3-sialyltransferase ST3Gal II (Siat5)	<i>Danio rerio</i>	n.d.	AJ783741 CAH04018.1		
$\alpha$ -2,3-sialyltransferase ST3Gal IV (Siat4c)	<i>Danio rerio</i>	n.d.	AJ744809 CAG32845.1		

FIGURE 9B

FIGURE 10B

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
$\alpha$ -2,6-sialyltransferase ST6GalNAc VI (Siat6)	<i>Danio rerio</i>	n.d.	AJ744801 CAG32837.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	<i>Danio rerio</i>	n.d.	AJ646874 CAG26703.1		
$\alpha$ -2,8-sialyltransferase ST8Sia I (Siat 8A) (fragment)	<i>Danio rerio</i>	n.d.	AJ715535 CAG29374.1		
$\alpha$ -2,8-sialyltransferase ST8Sia IV (Siat 8D) (fragment)	<i>Danio rerio</i>	n.d.	AJ715545 CAG29384.1		
$\alpha$ -2,8-sialyltransferase ST8Sia VI (Siat 8F) (fragment)	<i>Danio rerio</i>	n.d.	AJ715551 CAG29390.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc I (Siat6)	<i>Danio rerio</i>	n.d.	AJ619960 CAF04081.1		
$\alpha$ -2,6-sialyltransferase (CG4871) ST6Gal I	<i>Drosophila melanogaster</i>	2.4.99.1	AE003465 AAF47256.1 AF218237 AAG13185.1 AF397532 AAK92128.1 AE003465 AAM70791.1 NM_079129 NP_523853.1 NM_166684 NP_726474.1	Q9GU23 Q9W121	
$\alpha$ -2,3-sialyltransferase ST3Gal I	<i>Gallus gallus</i>	2.4.99.4	X80503 CAA56666.1 NM_205217 NP_990548.1	Q11200	
$\alpha$ -2,3-sialyltransferase (ST3GAL-II)	<i>Gallus gallus</i>	n.d.	AJ585761 CAE51385.2		
$\alpha$ -2,6-sialyltransferase ST6Gal I	<i>Gallus gallus</i>	2.4.99.1	X75558 CAA53235.1 NM_205241 NP_990572.1	Q92182	
$\alpha$ -2,6-sialyltransferase ST6GalNAc II	<i>Gallus gallus</i>	2.4.99.-	X77775 AAE68030.1 NM_205233 CAA54813.1 NP_990564.1	Q92184	

FIGURE 10C

12/23

FIGURE 10D

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB
$\alpha$ -2,3-sialyltransferase ST3Gal IV	<i>Homo sapiens</i>	2.4.99.-	L23767 AAA16460.1 AF036249 AAC14162.1 BC010645 AAH10645.1 AY040826 AAK93790.1 AF516602 AAM66431.1 AF516603 AAM66432.1 AF516604 AAM66433.1 AF525084 AAM81378.1 X74570 CAA52662.1 CR456858 CAG33139.1 NM_006278 NP_006269.1	Q11206 Q60497 Q96QQ9 Q8N6A6 Q8N6A7 Q8NFD3 Q8NFG7	1.3D
$\alpha$ -2,3-sialyltransferase ST3Gal IV	<i>Homo sapiens</i>	2.4.99.-	AF036249 AAC14162.1 BC010645 AAH10645.1 AY040826 AAK93790.1 AF516602 AAM66431.1 AF516603 AAM66432.1 AF516604 AAM66433.1 AF525084 AAM81378.1 X74570 CAA52662.1 CR456858 CAG33139.1 NM_006278 NP_006269.1	Q11206 Q60497 Q96QQ9 Q8N6A6 Q8N6A7 Q8NFD3 Q8NFG7	1.3D
$\alpha$ -2,6-sialyltransferase (ST6Gal II ; KIAA1877)	<i>Homo sapiens</i>	n.d.	BC008680 AAH08680.1 AB058780 BAB47506.1 AB059555 BAC24793.1 AJ512141 CAD54408.1 AX795193 CAE48260.1 AX795193 CAE48261.1 NM_032528 NP_115917.1	Q86Y44 Q8IUG7 Q96HE4 Q96JF0	
$\alpha$ -2,6-sialyltransferase (ST6GalNAc III)	<i>Homo sapiens</i>	n.d.	BC005068 AAH05068.1 AY058240 AAC08804.1 AK097684 CAC41111.1 AJ512141 CAD54408.1 NM_052996 NP_159445.1	Q8N289 Q8NBY1 Q8NBY1 Q8NBY1	
$\alpha$ -2,6-sialyltransferase (ST6GalNAc V)	<i>Homo sapiens</i>	n.d.	BC001201 AAH01201.1 AK056241 BAB71127.1 AL035409 CAB72344.1 AJ507292 CAD45372.1 NM_030965 NP_112227.1	Q9BVH7	
$\alpha$ -2,6-sialyltransferase (ST6GalNAc VI)	<i>Homo sapiens</i>	n.d.	BC004056 AAH04056.1 AJ261058 CAB31141.1 NM_006156 NP_006141.1	Q8HJ1 Q8HJ1 Q8HJ1	
$\alpha$ -2,6-sialyltransferase ST6Gal I	<i>Homo sapiens</i>	2.4.99.1	BC031476 AAH31476.1 BC040009 AAH40009.1 A17362 CAA01327.1 A23699 CAA01686.1 X17247 CAA35111.1 X54363 CAA38246.1 X62822 CAA44634.1 NM_003032 NP_003023.1 NM_173216 NP_775323.1	P15907	
$\alpha$ -2,6-sialyltransferase ST6GalNAc I	<i>Homo sapiens</i>	2.4.99.1	BC002182 AAH02182.1 AF006001 AAC02400.1 AY058913 AAC08917.1 AF006113 AAC00611.1 X17362 CAA01327.1 NM_001811 NP_001804.1	Q819N6 Q8N8C7 Q8N8C7 Q8N8C7 Q8N8C7 Q8N8C7	
$\alpha$ -2,8- polysialyltransferase ST8Sia IV	<i>Homo sapiens</i>	2.4.99.-	L41680 AAC41775.1 BC027866 AAH27866.1 BC053657 AAH53657.1 NM_005668 NP_005659.1	Q8N1F4 Q92187 Q92693	
$\alpha$ -2,8-sialyltransferase (polysialyltransferase ST8Sia)	<i>Homo sapiens</i>	2.4.99.1	L41680 AAC41775.1 BC027866 AAH27866.1 BC053657 AAH53657.1 NM_005668 NP_005659.1 L41680 AAC41775.1 BC027866 AAH27866.1 BC053657 AAH53657.1 NM_005668 NP_005659.1 L41680 AAC41775.1 BC027866 AAH27866.1 BC053657 AAH53657.1 NM_005668 NP_005659.1	Q86Y44 Q82187 Q93067 Q86Y44 Q82187 Q93067 Q86Y44 Q82187 Q93067 Q86Y44 Q82187 Q93067	
$\alpha$ -2,8-sialyltransferase	<i>Homo sapiens</i>	2.4.99.-	L29556 AAA36613.1	Q92186	



FIGURE 10E

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
ST8Sia II			U82762 AAB51242.1 U33551 AAC24458.1 BC069584 AAH69584.1 NM_006011 NP_006002.1	Q92470 Q92746	
$\alpha$ -2,8-sialyltransferase ST8Sia V	<i>Homo sapiens</i>	2.4.99.-	U91641 AAC51727.1 CR457037 CAG33318.1 NM_013305 NP_037437.1	O15466	
lactosylceramide $\alpha$ -2,3- sialyltransferase (ST3Gal V)	<i>Homo sapiens</i>	2.4.99.9	AF105026 AAD14634.1 AF119415 AAF66146.1 BC065936 AAH65936.1 AY152815 AAO16866.1 AAP65066 AAP65066.1 AY359105 AAQ89463.1 AB018356 BAA33950.1 AX876536 CAE89320.1 NM_003896 NP_003887.2	Q9UNP4 O94902	
<i>N</i> -acetylgalactosaminide $\alpha$ -2,6-sialyltransferase IV (ST6GalNAc IV)	<i>Homo sapiens</i>	2.4.99.-	AF127142 AAF00102.1 BC036705 AAH36705.1 -AAP63349.1 AB035172 BAA87034.1 AK000600 BAA91281.1 Y17461 CAB44354.1 AJ271734 CAC07404.1 AX061620 CAC24981.1 AX068265 CAC27250.1 AX969252 CAF14380.1 NM_014403 NP_055218.3 NM_175039 NP_778204.1	Q9H4F1 Q9NWU6 Q9UKU1 Q9ULB9 Q9Y3G3 Q9Y3G4	
unnamed protein product	<i>Homo sapiens</i>	n.d.	AK021929 BAB13940.1 AX881696 CAE91353.1	Q9HAA9	
unnamed protein product	<i>Homo sapiens</i>	n.d.	AK021929 BAB13940.1 AX881696 CAE91353.1	Q9HAA9	

FIGURE 35 10P

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
Gal $\beta$ -1,3/4-GlcNAc $\alpha$ -2,3-sialyltransferase (ST3Gal IV)	<i>Mesocricetus auratus</i>	2.4.99.6	AJ245700 CAB53395.1	Q9QXF5	
polysialyltransferase (ST8Sia IV)	<i>Mesocricetus auratus</i>	2.4.99.-	AJ245701 CAB53396.1	Q9QXF4	
$\alpha$ -2,3-sialyltransferase ST3Gal II	<i>Mus musculus</i>	2.4.99.4	BC015264 AAH15264.1 BC068064 AAH66064.1 AK034554 BAC28752.1 AK034863 BAC28859.1 AK053827 BAC35543.1 X76989 CAA54294.1 NM_009179 NP_033205.1 NM_178048 NP_835149.1	Q11204 Q8BPL0 Q8BSA0 Q8BSE9 Q91WH6	
$\alpha$ -2,3-sialyltransferase ST3Gal III	<i>Mus musculus</i>	2.4.99.4	BC006710 AAH106710.1 AK006050 BAB23729.1 AK013816 BAB21699.1 X81233 CAA59013.1 NM_009176 NP_033202.1	Q97325 Q91222 Q90721 Q91236 Q91236	
$\alpha$ -2,3-sialyltransferase ST3Gal IV	<i>Mus musculus</i>	2.4.99.4	BC011121 AAH11121.1 BC050773 AAH50773.1 D28941 BAA08068.1 AK008543 BAB25732.1 AB061305 BAB47508.1 X95809 CAA65076.1 NM_009178 NP_033204.2	P97354 Q81325 Q91Y74 Q921R5 Q9CVE8	
$\alpha$ -2,6-sialyltransferase ST6GalNAc II	<i>Mus musculus</i>	2.4.99.2	NM_009180 6677963 BC010208 AAH10208.1 AB027198 BAB00637.1 AK004613 BAB23410.1 X93999 CAA63821.1 X94000 CAA63822.1 NM_009180 NP_033206.2	P70277 Q9DC24 Q9JJM5	
$\alpha$ -2,6-sialyltransferase ST6Gal I	<i>Mus musculus</i>	2.4.99.2	BC024889 AAH24889.1 AB010665 BAB00665.1 AK034766 BAC28828.1 AK034122 BAC38120.1 NM_011598 NP_066604.1	Q64685 Q8BVB2 Q9JUI1 Q9JUI1 Q9JUI1	
$\alpha$ -2,6-sialyltransferase ST6Gal II	<i>Mus musculus</i>	n.d.	AK082586 BAC38534.1 AB095093 BAC87752.1 AK129482 BAC98272.1 NM_172829 NP_766417.1	Q8BUU4	
$\alpha$ -2,6-sialyltransferase ST6GalNAc III	<i>Mus musculus</i>	n.d.	BC058387 AAH58387.1 AK034804 BAC28836.1 Y11342 CAA72181.2 Y11343 CAB95031.1 NM_011372 NP_035502	Q9WUV2 Q9JHP5	
$\alpha$ -2,6-sialyltransferase ST6GalNAc IV	<i>Mus musculus</i>	2.4.99.7	BC056456 AAH56456.1 AK086730 BAC39623.1 AK008100 CAA07461.1 NM_016790 NP_066607.1	Q8C392 Q9JHP2 Q9R2B6 Q8B722	

FIGURE 56 106

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
$\alpha$ -2,8-sialyltransferase (GD3 synthase) ST8Sia I	<i>Mus musculus</i>	2.4.99.8	L38677 AAA91869.1 BC024821 AAH24821.1 AK048188 BAC32625.1 AK052444 BAC34994.1 X84235 CAA59014.1 AJ401102 CAC20706.1 NM_011374 NP_035504.1	Q64468 Q64687 Q8BL76 Q8BWI0 Q8K1C1 Q9EPK0	
$\alpha$ -2,8-sialyltransferase ST8Sia II	<i>Mus musculus</i>	2.4.99.-	X83562 CAA58548.1 X99646 CAA67965.1 X99647 CAA67965.1 X99648 CAA67965.1 X99649 CAA67965.1 X99650 CAA67965.1 X99651 CAA67965.1 NM_009181 NP_033207.1	O35696	
$\alpha$ -2,8-sialyltransferase ST8Sia V	<i>Mus musculus</i>	2.4.99.-	BC006112 AAH06112.1 AK006993 BAC22993.1 AK006723 BAC20673.1 X92299 CAA61168.1 X98690 CAA66690.1 X99434 CAA67069.1 NM_009181 NP_033207.1	Q64692 Q8B770 Q8B770 Q8B770 Q8B770 Q8B770	
$\alpha$ -2,8-sialyltransferase ST8Sia V	<i>Mus musculus</i>	2.4.99.-	BC034855 AAH34855.1 AK078670 BAC37354.1 X98014 CAA66642.1 X98014 CAA66643.1 X98014 CAA66644.1 NM_013666 NP_038694.1 NM_153124 NP_094764.1 NM_177416 NP_803135.1	P70126 P70127 P70128 Q8BJW0 Q8JZQ3	
$\alpha$ -2,8-sialyltransferase ST8Sia III	<i>Mus musculus</i>	2.4.99.-	BC077562 BAAH7562.1 AK016574 BAC39974.1 X86002 CAA59665.1 NM_009181 NP_033207.1	Q64689 Q8C406 Q8C406	
GD1 synthase (ST6GalNAc V)	<i>Mus musculus</i>	n.d.	BC055737 AAH55737.1 AB030836 BAA85747.1 AB028840 BAA89292.1 AK034387 BAC28693.1 AK038434 BAC29997.1 AK042683 BAC31331.1 NM_012028 NP_036158.2	Q8CAM7 Q8CBX1 Q9QYJ1 Q9R0K8	
GMP synthase $\alpha$ -2,8-sialyltransferase ST6GalNAc VI	<i>Mus musculus</i>	2.4.99.9	BC016916 AAH16916.1 X83562 CAA58548.1 AB018045 BAA38497.1 AB018302 BAA38497.1 AK022861 BAC28671.1 X15690 CAA73235.1 NM_011374 NP_035504.1	Q88129 Q8C255 Q9QWV6 Q9QWV6 Q9QWV6 Q9QWV6	
N-acetylgalactosaminide $\alpha$ -2,6-sialyltransferase (ST6GalNAc VI)	<i>Mus musculus</i>	2.4.99.-	BC036985 AAH36985.1 AB035174 BAA87036.1 AB035123 BAA95940.1 AK030648 BAC27064.1 NM_016973 NP_058669.1	Q8CDC3 Q8JZW3 Q9JM95 Q9R0G9	
$\alpha$ -2,3-sialyltransferase	<i>Oncorhynchus</i>	n.d.	AJ585760 CAE51384.1		



FIGURE 10

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB
(ST3Gal-I)	<i>mykiss</i>				
$\alpha$ -2,8-polysialyltransferase IV (ST8Sia IV)	<i>Oncorhynchus mykiss</i>	n.d.	AB094402 BAC77411.1	Q7T2X5	
$\alpha$ -2,3-sialyltransferase ST3Gal IV	<i>Oryctolagus cuniculus</i>	2.4.99.-	AF121967 AAF28871.1	Q9N257	
$\alpha$ -2,3-sialyltransferase ST3Gal IV	<i>Oryza sativa (japonica cultivar-group)</i>	n.d.	AL731626 CAD41185.1 AL662969 CAE04714.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	<i>Oryzias latipes</i>	n.d.	AJ646876 CAG26705.1		
$\alpha$ -2,3-sialyltransferase ST3Gal II (Siat5)	<i>Pan troglodytes</i>	n.d.	AJ744804 CAG32840.1		
$\alpha$ -2,3-sialyltransferase ST3Gal IV (Siat4c)	<i>Pan troglodytes</i>	n.d.	AJ626824 CAF25182.1		
$\alpha$ -2,6-sialyltransferase (Siat7A)	<i>Pan troglodytes</i>	n.d.	AJ748740 CAG38615.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc III (Siat7C)	<i>Pan troglodytes</i>	n.d.	AJ634454 CAG25676.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc IV (Siat7D) (fragment)	<i>Pan troglodytes</i>	n.d.	AJ646875 CAG26704.1		
$\alpha$ -2,8-sialyltransferase 8A (Siat8A)	<i>Pan troglodytes</i>	2.4.99.8	AJ697658 CAG26896.1		
$\alpha$ -2,8-sialyltransferase 8C (Siat8C)	<i>Pan troglodytes</i>	n.d.	AJ697660 CAG26898.1		
$\alpha$ -2,8-sialyltransferase 8D (Siat8D)	<i>Pan troglodytes</i>	n.d.	AJ697662 CAG26900.1		
$\alpha$ -2,8-sialyltransferase 8E (Siat8E)	<i>Pan troglodytes</i>	n.d.	AJ697663 CAG26901.1		
$\beta$ -galactosamide $\alpha$ -2,6-sialyltransferase I (ST6Gal I; Siat1)	<i>Pan troglodytes</i>	2.4.99.1	AJ627624 CAF29492.1		
$\beta$ -galactosamide $\alpha$ -2,6-sialyltransferase II (ST6Gal II; Siat2)	<i>Pan troglodytes</i>	n.d.	AJ627625 CAF29493.1		
GM3 synthase ST3Gal V	<i>Pan troglodytes</i>	n.d.	AJ744807 CAG32843.1		

FIGURE 9 10 E

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
(Slat9)					
$\alpha$ -2,3-sialyltransferase ST3Gal III	<i>Rattus norvegicus</i>	2.4.99.6	M97754 AAA42146.1 NM 031687 NP 113885.1	Q02734	
$\alpha$ -2,3-sialyltransferase ST3Gal IV (Slat9)	<i>Rattus norvegicus</i>	n.d.	AJ626825 CAG25180.1		
$\alpha$ -2,3-sialyltransferase ST3Gal VI	<i>Rattus norvegicus</i>	n.d.	AJ626743 CAG25053.1		
$\alpha$ -2,6-sialyltransferase ST6Gal I	<i>Rattus norvegicus</i>	2.4.99.1	M18769 AAA41196.1 M83143 AAB07233.1	P13721	
$\alpha$ -2,6-sialyltransferase ST6GalNAc I (Slat7A)	<i>Rattus norvegicus</i>	n.d.	AJ634458 CAG25680.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc II (Slat7B)	<i>Rattus norvegicus</i>	n.d.	AJ634457 CAG25679.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc III (Slat7C)	<i>Rattus norvegicus</i>	2.4.99.6	L29555 AAG19086.1 U067240 AAF17240.1 NM 009123 NP 001996.1	Q06168	
$\alpha$ -2,6-sialyltransferase ST6GalNAc IV (Slat7D) (fragment)	<i>Rattus norvegicus</i>	n.d.	AJ646871 CAG26700.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Slat7E)	<i>Rattus norvegicus</i>	n.d.	AJ646872 CAG26701.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc VI (Slat7F) (fragment)	<i>Rattus norvegicus</i>	n.d.	AJ646881 CAG26710.1		
$\alpha$ -2,8-sialyltransferase ST8Sia I	<i>Rattus norvegicus</i>	2.4.99.6	U05088 AAC27414.1 U047265 BAA08218.1	P70557 Q09742	
$\alpha$ -2,8-sialyltransferase (SIAT8E)	<i>Rattus norvegicus</i>	n.d.	AJ699422 CAG27884.1		
$\alpha$ -2,8-sialyltransferase ST8Sia II	<i>Rattus norvegicus</i>	2.4.99.-	L13445 AAA42147.1 NM 057156 NP 476497.1	Q07977 Q64688	
$\alpha$ -2,8-sialyltransferase ST8Sia III	<i>Rattus norvegicus</i>	2.4.99.-	U05088 BAA08218.1 NM 001362 NP 007161.1	P70557 Q08563	
$\alpha$ -2,8-sialyltransferase ST8Sia IV	<i>Rattus norvegicus</i>	2.4.99.-	U90215 AAB49989.1	O08563	
$\alpha$ -2,6-sialyltransferase GM3 synthase ST3Gal V	<i>Rattus norvegicus</i>	n.d.	AJ627026 CAG29494.1 AB018049 BAA33492.1 NM 031337 NP 112627.1	O88830	
$\alpha$ -2,3-sialyltransferase ST3Gal V (Slat7A)	<i>Rattus norvegicus</i>	n.d.	AJ627026 CAG29494.1		
$\alpha$ -2,3-sialyltransferase (ST3Gal-II)	<i>Silurana tropicalis</i>	n.d.	AJ585763 CAE51387.1		
$\alpha$ -2,6-sialyltransferase (ST6GalNAc)	<i>Strongylocentrotus purpuratus</i>	n.d.	AJ626850 CAG05649.1		
$\alpha$ -2,3-sialyltransferase ST3Gal II (Slat7B)	<i>Strongylocentrotus purpuratus</i>	n.d.	AJ585763 CAE51389.1		
$\alpha$ -2,3-sialyltransferase (ST3Gal-IV)	<i>Sus scrofa</i>	n.d.	AJ584674 CAE48299.1		
$\alpha$ -2,3-sialyltransferase ST3Gal I (Slat7C)	<i>Sus scrofa</i>	2.4.99.4	M97753 AAA42145.1	Q02748	
$\alpha$ -2,6-sialyltransferase (fragment) ST6Gal I	<i>Sus scrofa</i>	2.4.99.1	AF136746 AAD33059.1	Q9XSG8	
$\alpha$ -2,6-sialyltransferase (fragment) ST6Gal I	<i>Sus scrofa</i>	n.d.	AJ620948 CAG06585.2		
$\alpha$ -2,6-sialyltransferase (fragment) ST6Gal I	<i>Sus scrofa</i>	n.d.	AF041031 AAC15633.1	O62717	

FIGURE 9

10J

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
$\alpha$ -2,3-sialyltransferase (Siat5-r)	<i>Takifugu rubripes</i>	n.d.	AJ744805 CAG32841.1		
$\alpha$ -2,3-sialyltransferase (Siat5)	<i>Takifugu rubripes</i>	n.d.	AJ626815 CAF25175.1		
$\alpha$ -2,3-sialyltransferase ST3Gal II (Siat5) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ626817 CAF25175.1		
$\alpha$ -2,3-sialyltransferase ST3Gal III (Siat6)	<i>Takifugu rubripes</i>	n.d.	AJ626818 CAF25176.1		
$\alpha$ -2,6-sialyltransferase ST6Gal I (Siat1)	<i>Takifugu rubripes</i>	n.d.	AJ744800 CAG32836.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc II (Siat7B)	<i>Takifugu rubripes</i>	n.d.	AJ634460 CAG25681.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc II B (Siat7B-related)	<i>Takifugu rubripes</i>	n.d.	AJ634461 CAG25682.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc III (Siat7C) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ634465 CAG25687.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc IV (Siat7D) (fragment)	<i>Takifugu rubripes</i>	2.4.99.3	Y17466 CAB44338.1 AJ646869 CAG26698.1	Q9W6U6	
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ646870 CAG26700.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc VI (Siat7F) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ646880 CAG26709.1		
$\alpha$ -2,8-sialyltransferase ST8Sia I (Siat8A) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ715534 CAG29373.1		
$\alpha$ -2,8-sialyltransferase ST8Sia II (Siat 8B) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ715538 CAG29377.1		
$\alpha$ -2,8-sialyltransferase ST8Sia III (Siat8C) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ715541 CAG29380.1		
$\alpha$ -2,8-sialyltransferase ST8Sia IIIr (Siat 8Cr)	<i>Takifugu rubripes</i>	n.d.	AJ715542 CAG29381.1		
$\alpha$ -2,8-sialyltransferase ST8Sia IV (Siat 8D) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ715547 CAG29386.1		
$\alpha$ -2,8-sialyltransferase ST8Sia VI (Siat 8F) (fragment)	<i>Takifugu rubripes</i>	n.d.	AJ715549 CAG29388.1		
$\alpha$ -2,8-sialyltransferase ST8Sia VII (Siat8G)	<i>Takifugu rubripes</i>	n.d.	AJ715550 CAG29389.1		
$\alpha$ -2,3-sialyltransferase (Siat5-r)	<i>Tetraodon nigroviridis</i>	n.d.	AJ744806 CAG32842.1		
$\alpha$ -2,3-sialyltransferase ST3Gal I (Siat4)	<i>Tetraodon nigroviridis</i>	n.d.	AJ744807 CAG32838.1		
$\alpha$ -2,3-sialyltransferase ST3Gal III (Siat6)	<i>Tetraodon nigroviridis</i>	n.d.	AJ626822 CAF25180.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc II (Siat7B)	<i>Tetraodon nigroviridis</i>	n.d.	AJ684462 CAG25683.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	<i>Tetraodon nigroviridis</i>	n.d.	AJ646879 CAG26708.1		
$\alpha$ -2,8-sialyltransferase ST8Sia I (Siat8A) (fragment)	<i>Tetraodon nigroviridis</i>	n.d.	AJ715536 CAG29375.1		
$\alpha$ -2,8-sialyltransferase ST8Sia II (Siat 8B) (fragment)	<i>Tetraodon nigroviridis</i>	n.d.	AJ715537 CAG29376.1		
$\alpha$ -2,8-sialyltransferase ST8Sia III (Siat 8C) (fragment)	<i>Tetraodon nigroviridis</i>	n.d.	AJ715539 CAG29378.1		

FIGURE 9A 10 K

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
$\alpha$ -2,8-sialyltransferase ST8Sia IIr (Siat 8Cr) (fragment)	<i>Tetraodon nigrovittatus</i>	n.d.	AJ715540 CAG29379.1		
$\alpha$ -2,3-sialyltransferase (St3Gal-II)	<i>Xenopus laevis</i>	n.d.	AJ585762 CAE51386.1		
$\alpha$ -2,3-sialyltransferase St3Gal-III (Siat6)	<i>Xenopus laevis</i>	n.d.	AJ585764 CAE51388.1 AJ626823 CAF25181.1		
$\alpha$ -2,8-sialyltransferase ST8Sia-I (Siat8A;GD3 synthase)	<i>Xenopus laevis</i>	n.d.	AY272056 AAQ18162.1 AY272057 AAQ18163.1 AJ704562 CAG28695.1		
$\alpha$ -2,3-sialyltransferase (3Gal-VI)	<i>Xenopus tropicalis</i>	n.d.	AJ626744 CAF25054.1		
$\alpha$ -2,6-sialyltransferase ST6GalNAc V (Siat7E) (fragment)	<i>Xenopus tropicalis</i>	n.d.	AJ646878 CAG26707.1		
$\beta$ -galactosamide $\alpha$ -2,6- sialyltransferase II (ST6Gal II)	<i>Xenopus tropicalis</i>	n.d.	AJ627628 CAF29496.1		
polysialyltransferase	<i>Escherichia coli K92</i>	2.4.-.-	M88479 AAA24215.1 Q47404		
SynE	<i>Neisseria meningitidis FAM18</i>	n.d.	U75650 AAB53842.1 O06435		
SiaD (fragment)	<i>Neisseria meningitidis M209</i>	n.d.	AY281046 AAP34769.1		
polysialyltransferase (SiaD)(fragment)	<i>Neisseria meningitidis M3315</i>	n.d.	AY234191 AAO85289.1		
polysialyltransferase (SiaD)(fragment)	<i>Neisseria meningitidis M4211</i>	n.d.	AY234190 AAO85288.1		
polysialyltransferase (SiaD)(fragment)	<i>Neisseria meningitidis M5177</i>	n.d.	AY234193 AAO85291.1		
SiaD (fragment)	<i>Neisseria meningitidis M980</i>	n.d.	AY281045 AAP34768.1		



FIGURE 10L

Protein	Organism	EC#	GenBank / GenPept	SwissProt / PDB
ORF2	<i>Haemophilus influenzae A2</i>	n.d.	M94855 AAA24979.1	
$\alpha$ -2,3-sialyltransferase	<i>Neisseria gonorrhoeae F62</i>	2.4.99.4	U60664 AAC44539.1 AAE67205.1	P72074
$\alpha$ -2,3-sialyltransferase	<i>Neisseria meningitidis 406Y, NRCC 4030</i>	2.4.99.4	U60661 AAC44543.1	
$\alpha$ -2,3-sialyltransferase	<i>Neisseria meningitidis Z2491</i>	n.d.	AL162755 CAB84380.1 NC_003116 NP_283887.1	Q9JUV5
WaaH	<i>Salmonella enterica SARB25</i>	n.d.	AF519787 AAM82550.1	Q8KS93
WaaH	<i>Salmonella enterica SARB39</i>	n.d.	AF519789 AAM82552.1	
WaaH	<i>Salmonella enterica SARB57</i>	n.d.	AF519791 AAM82554.1	Q8KS91
WaaH	<i>Salmonella enterica SARB71</i>	n.d.	AF519793 AAM82556.1	Q8KS89
WaaH	<i>Salmonella enterica SARB88</i>	n.d.	AF519792 AAM82555.1	Q8KS90
WaaH (fragment)	<i>Salmonella enterica SARC10</i>	n.d.	AF519785 AAM88840.1	Q8KS98
WaaH (fragment)	<i>Salmonella enterica SARC12</i>	n.d.	AF519781 AAM88842.1	
WaaH (fragment)	<i>Salmonella enterica SARC13</i>	n.d.	AF519782 AAM88843.1	Q8KS96
WaaH (fragment)	<i>Salmonella enterica SARC14I</i>	n.d.	AF519783 AAM88844.1	Q8KS97
WaaH	<i>Salmonella enterica SARC16II</i>	n.d.	AF519784 AAM88845.1	Q8KS95

FIGURE 10M

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
WaaH (fragment)	<i>Salmonella enterica</i> SARC4I	n.d.	AF519773 AAM88835.1	Q8KSA3	
WaaH	<i>Salmonella enterica</i> SARC6IIa	n.d.	AF519775 AAM88837.1	Q8KSA2	
WaaH	<i>Salmonella enterica</i> SARC9V	n.d.	AF519778 AAM88839.1	Q8KSA0	
bifunctional $\alpha$ -2,3/2,8-sialyltransferase (Cst-II)	<i>Campylobacter jejuni</i> ATCC 33291	n.d.	AF101520 AAL06004.1	Q93C	
Cst	<i>Campylobacter jejuni</i> 81-176	n.d.	AF305571 AAL09368.1		
$\alpha$ -2,3-sialyltransferase (Cst-II)	<i>Campylobacter jejuni</i> ATCC 43430	2.4.99.-	AF400047 AAK85419.1		
$\alpha$ -2,3/8-sialyltransferase (CstII)	<i>Campylobacter jejuni</i> ATCC 43438	n.d.	AF400048 AAK91725.1	Q93MQ0	
$\alpha$ -2,3-sialyltransferase (Cst-II)	<i>Campylobacter jejuni</i> ATCC 43456	2.4.99.-	AF401528 AAL05990.1	Q93D05	
$\alpha$ -2,3/8-sialyltransferase (Cst-II)	<i>Campylobacter jejuni</i> ATCC 700297	n.d.	AF216647 AAL36462.1		
$\alpha$ -2,3-sialyltransferase cstIII	<i>Campylobacter jejuni</i> MSC57360	2.4.99.-	AF195055 AAG29922.1		
$\alpha$ -2,3/8-sialyltransferase (CstII)	<i>Campylobacter jejuni</i> O:10	n.d.	-AAO98669.1 AX934427 CAF04167.1		
$\alpha$ -2,3/8-sialyltransferase (CstII)	<i>Campylobacter jejuni</i> O:36	n.d.	AX934436 CAF04171.1		
$\alpha$ -2,3/8-sialyltransferase (CstII)	<i>Campylobacter jejuni</i> O:41	n.d.	-AAO98670.1 -AAT17967.1 AX934429 CAF04168.1		
bifunctional $\alpha$ -2,3/2,8-sialyltransferase (Cst-II)	<i>Campylobacter jejuni</i> OH4384	2.4.99.-	AF130984 AAF31771.1 AX934425 CAF04166.1	1RO7 C 1RO8 A	

## FIGURE 4

ION

Protein	Organism	EC#	GenBank / GenPept	SwissProt	PDB / 3D
PM1174	<i>Pasteurella multocida</i>	n.d.	AE008167 AAK03258.1 NC 002683 NP_248111.1	Q9CLP3	
Sequence 10 from patent US 6699705	Unknown.	n.d.		-AAT17969.1	
Sequence 2 from patent US 6709834	Unknown.	n.d.		-AAT23232.1	
Sequence 3 from patent US 6699705	Unknown.	n.d.		-AAT17965.1	
Sequence 35 from patent US 6503744 (fragment)	Unknown.	n.d.		-AAO96685.1 -AAS36262.1	
Sequence 5 from patent US 6699705	Unknown.	n.d.		-AAT17966.1	